

**SUPPLEMENTAL EXPERIMENTAL PROCEDURES:****Analysis of RNA-seq data**

Two replicates of long RNA-seq experiments from ENCODE/Cold Spring Harbor Lab corresponding to mouse heart, thymus and small intestine were downloaded from UCSC genome browser and used as input for *Cufflinks* for transcript assembly and *Cuffmerge* to obtain the presented RNA-seq data track.

**Affymetrix microarray hybridization and data analysis**

Cells were harvested with TRIzol Reagent (Invitrogen) and RNA extracted according to the manufacturer's instructions followed by purification with the RNeasy Mini-kit (Qiagen, Hilden, Germany). Before cDNA synthesis, RNA integrity from each sample was confirmed on Agilent RNA Nano LabChips (Agilent Technologies). The sense cDNA was prepared from 300 ng of total RNA using the Ambion® WT Expression Kit. The sense strand cDNA was then fragmented and biotinylated with the Affymetrix GeneChip® WT Terminal Labeling Kit (PN 900671). Labeled sense cDNA was hybridized to the Affymetrix Mouse Gene 1.0 ST microarray according to the manufacturer protocols and using GeneChip® Hybridization, Wash and Stain Kit. Genechips were scanned with the Affymetrix GeneChip® Scanner 3000.

Both background correction and normalization were done using RMA (Robust Multichip Average) algorithm [1]. Then, a filtering process was performed to eliminate low expression probe sets. Applying the criterion of an expression value greater than 64 in at least two samples for each experimental condition (siRNA\_Control, siRNA\_P53, ASO\_Control, ASO\_Pint), 21553 probe sets were selected for statistical analysis. R/Bioconductor [2] was used for preprocessing and statistical analysis. LIMMA (Linear Models for Microarray Data) [3] was used to find out the probe sets that showed significant differential expression between experimental conditions. Genes were

selected as significant using criteria based on a combination of B statistic and log fold-change cut offs specific for each contrasts.

### ChiP-seq analysis

For generation of average aggregate plots, the proceseed ChIP-Seq datasets for H3K4me3 y H3K27me3 histone modifications of murine ES cell lines were downloaded from the public database GEO (accession number GSE8024). Briefly, reads were aligned to the reference genome, and the fragment count at any given position was estimated as the number of uniquely aligned reads oriented towards it and within 300 bp (Mikkelsen et al. 2007). Composite profile of the promoters of *PINT* genes, Suz12 genes and *PINT*+Suz12 genes were calculated considering the TSS annotated in the reference genome. The plots obtained show mean ChIP-Seq fragment densities of H3K4me3 and H3K27me3 over all analyzed promoters.

### Agilent microarray data analysis

Total RNA from human tissue samples was extracted with TRIzol Reagent (Invitrogen) according to the manufacturer's instructions, followed by purification with the RNeasy Mini-kit (Qiagen, Hilden, Germany). Before cDNA synthesis, RNA integrity from each sample was confirmed on Agilent RNA Nano LabChips (Agilent Technologies). RNA was hybridized to Agilent® SurePrint G3 Human GE 8x60 Microarray catalog # G4858A-028004.

Data normalization and analysis was performed using GiTools application [4]. For the correlation analysis first a z-score median enrichment analysis was carried out using KEGG pathway modules and the microarray data. The obtained z-scores matrix, representing the enrichment level of pathways in the samples, was then attached to an expression level matrix containing the lincRNA probes. With this resulting matrix a Pearson's correlation coefficient analysis was performed.

## Functional and pathway analysis

Functional enrichment analysis of Gene Ontology (GO) categories was carried out using standard hypergeometric test [5]. The biological knowledge extraction was complemented through the use of Ingenuity Pathway Analysis (Ingenuity Systems, www.ingenuity.com), which database includes manually curated and fully traceable data derived from literature sources.

## SUPPLEMENTAL MATERIALS:

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#### Antibodies

ANTIBODIES	SUPPLIER	CAT.#	USE
<i>Suz12</i>	Abcam	ab12073	RIP-WB, RNA PULL DOWN
<i>IgG rabbit</i>	Cell Signaling	2729S	RIP & ChIP
<i>Wdr5</i>	Abcam	ab56919	RIP
<i>Suz12</i>	Bethyl	A302-407A	ChIP
<i>H3K27me3</i>	Abcam	ab6002	ChIP
<i>p53 (CM5)</i>	Novocastra	NCL-p53-CM5p	WB&ChIP
<i>p53 (DO-1)</i>	Santa Cruz	sc126	WB&ChIP
<i>Ezh2</i>	Cell Signaling	ac22	WB
<i>Beta-tubulin</i>	Sigma	T5293	WB

#### Oligonucleotides

Antisense Oligos (ASOs)	sequence	Position
ASO #1	GCCGACTCCCCATCTCTGCC	ex4
ASO #2	GGCACCCATCTCCCTGCAA	intronic
ASO #3	TAGCTCAGTTCTTAACGC	ex3
ASO #4	CCTTAGTTAGCTTGGTCT	intronic
ASO CTRL #1	CCTTCCCTGAAGGTTCCCTCC	
ASO CTRL #2	TAGTGCAGGACCTACCCACGA	

siRNA	sequence	Supplier
siRNA <i>p53</i> #1	AGAAGAAAAUUUUCGCAAA	Ambion
siRNA <i>p53</i> #2	ACAGCGUGGUGGUACCUUA	Ambion
siRNA control	Not available from supplier	Ambion

	FORWARD	REVERSE
<b>shRNA cloning</b>		
<i>Ezh2</i>	CCGGCGGCTCCTCTAACCATGTTACT	AATTCAAAAACGGCTCCTCTAACCATG
Scramble	CCGGCAACAGCCACAACGTCTATATCT	AATTCAAAAACAACAGCCACAACGTCT

## qRT-PCR and qPCR primers

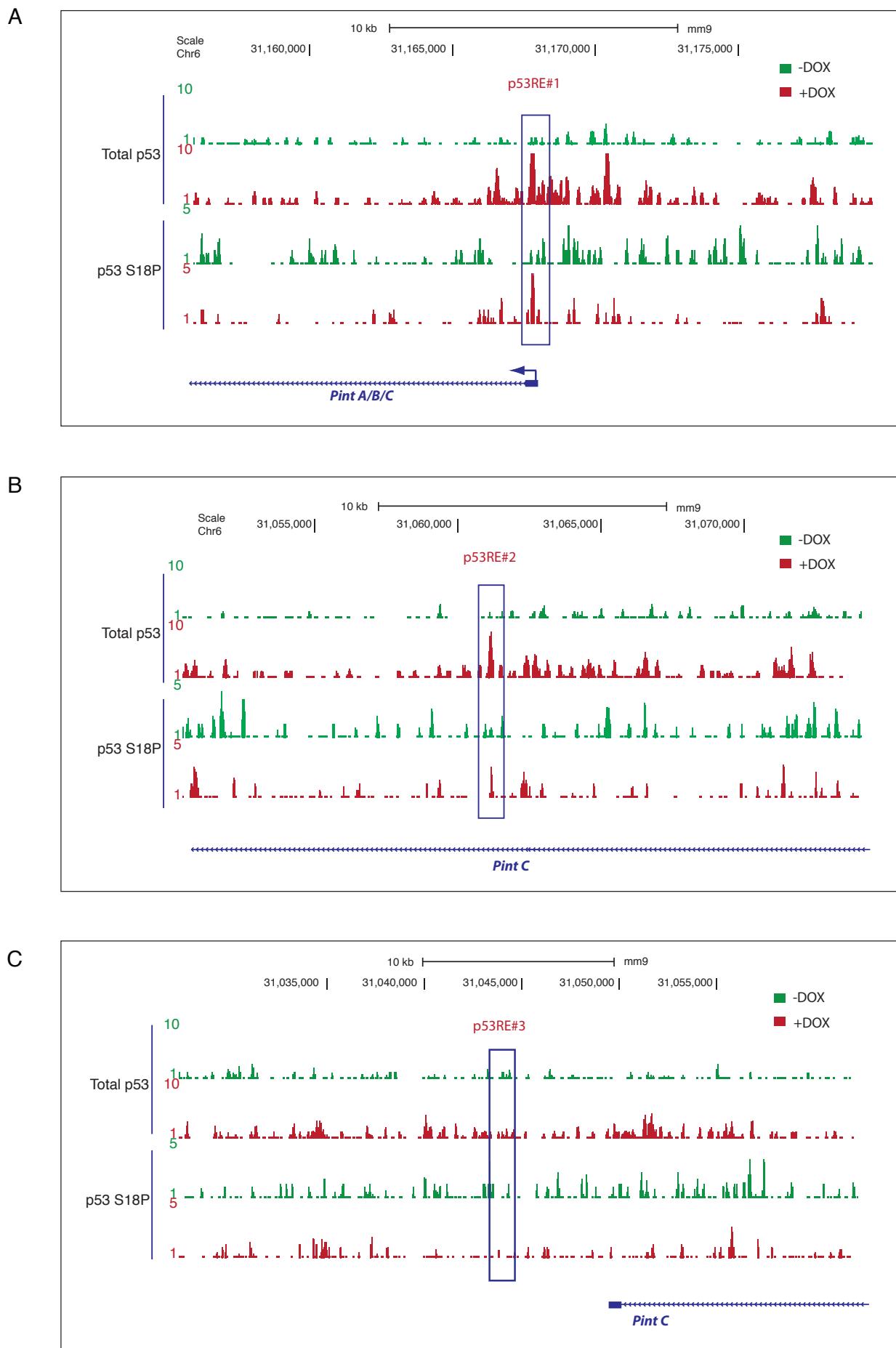
GENE	FORWARD	REVERSE	FIGURE
<b>mouse qPCR</b>			
<i>Gapdh</i>	GGGAAATTCAACGGCACAGT	AGATGGTGATGGGCTTCCC	1E, 1F, 1G, 2A, 2C, 3C, 4A, S2B, S2C, S2D, S3A, S3H, S4C, S5F, S5G
<i>Pint A.1</i>	CGCGCACGTATTCTGTATG	AGGAACCCGAAAGACACCTT	S3B
<i>Pint A.2</i>	CGGTGTAGTGTTCAGCCTCA	GGTGGCAGACTCCTGTTAGC	1E, 1F, 1G, 2A, 2C, 3C, 4A, 4D, S2C, S2D, S3A, S3H, S4C, S5G
<i>Pint C</i>	GACCAGGTTGCTGCTATTCTTC	AAGGCTGCACAGATACTGACT	S2B
<i>Pint B</i>	CGGTGTAGTGTTCAGCCTCA	TGGCTCTGATCTGTGGTCA	S2B
<i>Ezh2</i>	CTCTTCTGTCGACGATGTTTAAG	GGGTGTTGCATGGAAGGA	S5F
<i>U1</i>	GATCACGAAGGTGGTTTCC	TAAAGGGGAGAGCACAAACG	4A
<i>Arc</i>	GGTAGCTGAAGGCCAAAT	TTCACTGGTATGAATCACTGCTG	S4C
<i>Gadd45b</i>	CTGCCTCCTGGTCACGAA	TTGCCTCTGCTCTTCACA	S4C
<i>Celf5</i>	GGGACCAAGGGACAGACAG	CTGGAGGTATATGGTGTGACG	S4C
<i>Mmp15</i>	GCCTGCAGCTCTTCCTC	CCCTTGGCCTAGGTGAGA	S4C
<i>Egr2</i>	CTCCAGGTAGCGAGGGAGTT	CCTTGGCGGTATCATCTT	S4C
<i>Nkx2-9</i>	GTGCGTCCACAGACTGCT	GAGTCTGCAGGGCTGTCTC	S4C
<i>Atm</i>	CCCCACCCCTGATAAGCAAG	CTCTGGCCCTCAACACGAT	S4C
<i>Angpt2</i>	GATCAGACCAGTGAAATAAACAAAGC	GAGCTCTGCTGGACACCA	S4C
<i>Amigo2</i>	GCTGTATCTCCAACAAAGA	CTTGGCTGAATCTGGATAAG	S4C
<i>Serpina3N</i>	CTTCGCCACAACACATCAC	CTCTTACCGACTTCAGCCTATT	S4C
<i>Fas</i>	TGTCAACCATGCCAACCT	CCCTTCTCCAATTCTCTTCTT	S4C
<i>Il1r1</i>	AGGTGGAGGACTCAGGATATT	CCAGGGTCATTCTCTAACACAG	S4C
<i>Pik3r1</i>	CCAGTCCCTGACTCAAGAATTA	CCCTGTACCAAAGCACTATGT	S4C
<i>Jag2</i>	GACAATGACACCACTCCAGATG	CATCACACGCGTACTCGGATCT	S4C
<i>Tgfbi</i>	CAGTGGTACAGAGGAAGA	CAGATTGAGAGCGGAAGAG	S4C
<i>p53</i>	ACGTTCTCCGAAGACTGG	AGGGAGCTCGAGGCTGATA	S2B

ChIP p53 qPCR mouse	FORWARD	REVERSE	FIGURE
<i>Pint p53RE#1</i>	TCCTCTGGAGTGAGGAGGAA	CCTGTCTCAGAGTCCCCATC	1C
<i>Pint p53RE#2</i>	TGCACTGCTATGAACCTGGTT	GTGACCCAGCAAGTCATTGG	1C
<i>Pint p53RE#3</i>	CCAGCTCAGCTCTGAGTCAC	GCTTCACGAGGAGACTGGT	1C
<i>Cdkn1a p53RE</i>	GAGACCAGCAGCAAAATCG	CAGCCCCACCTCTCAATT	1C
<i>Nc6 (control-)</i>	GCTCCCTCAGCTTCAACATC	CAGAGTGATGAAAGGGTGG	1C

ChIP Suz12 qPCR	FORWARD	REVERSE	FIGURE
<i>Gm1337</i>	CCCTCGGGATGAGGACTAA	CCAAACTCACCCAGTCTTC	5D,5E, S5B, S5C
<i>Hoxc11</i>	TGTCTGCTACCTCTACGGG	AATGCTTCTGCAAATCCAGG	5D,5E, S5B, S5C
<i>Chd7</i>	TCTGAAACCAGGCAGATT	GTGCTGAGCTCCATGTGAAA	5D,5E, S5B, S5C
<i>Lrp2</i>	CTCGTGCATGCTCTCACC	AGCGTGGGAGGCAGTTT	5D,5E, S5B, S5C
<i>Kdr</i>	AAGTCACAGAGGCGGTATGC	AACCTGGCTGACCCGATT	5D,5E, S5B, S5C
<i>Rab20</i>	AAGACTCGGCAGGGTAAAG	AGGCAGCTGGGAAGTAGAGTT	5D,5E, S5B, S5C
<i>Chd6</i>	GGCAGGAAAAATAAAAGTTAAGAG	TGAGCTAAACTCACCAATAATA	5D,5E, S5B, S5C
<i>Frmda</i>	AAG	GC	
<i>Foxq1</i>	GGTGTTGTTGTTGAGCA	AAGGCAGAGACCGTACAGTTG	5D,5E, S5B, S5C
<i>Tll2</i>	CTCGGCCTAACGCCCTTTAG	CTGGTAGAGCTGACACTTTTGG	5D,5E, S5B, S5C
<i>Hey1</i>	GCCAATCACTTATGCGTCCT	GGGTTCCCTCGAAGTTACG	5D,5E, S5B, S5C
<i>Rasgrf2</i>	GGCGCTTCTCGATGATCT	TCATAACGTAATGCCCTCCTT	5D,5E, S5B, S5C
<i>Elovl3.F1</i>	GATGGTATGGAACCACTCTC	5D,5E, S5B, S5C	
<i>4930486G11Rik</i>	GGGCAAACTGGTCTTAGG	CGATGATGGTAGAACTGACTG	
<i>Nefm</i>	TGCCTGCTCTGTACTC	CCCTCAGCAGTTATCCAATC	5D,5E, S5B, S5C
<i>Tmem171</i>	CAAGCCTGCGGTGATT	GCGACCTACTTACAGGTAAG	5D,5E, S5B, S5C
<i>Gpr84</i>	AAGGAGCTGGTCCCTAG	5D,5E, S5B, S5C	
<i>Hcn1</i>	GTGAGGATGGAGACAGAATTG	TTTCCTGCTCCTCTCCA	5D,5E, S5B, S5C
<i>Sox1</i>	GGGCAAGGAGACTTCGAG	5D,5E, S5B, S5C	
<i>Nxph4.F1</i>	ACAGGAACGGAGACTTCGAG	CCACTTCTGGGTCTGAAGC	5D,5E, S5B, S5C
<i>Bmp3.F1</i>	GGGGCTTGAGGAGGGTAAG	5D,5E, S5B, S5C	
	GCTGCTCTGTCTATGGCTAGG	GTGCAAGTTGGTCTGTCC	5D,5E, S5B, S5C

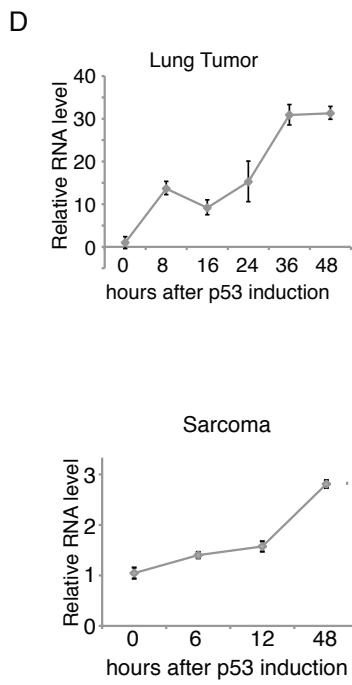
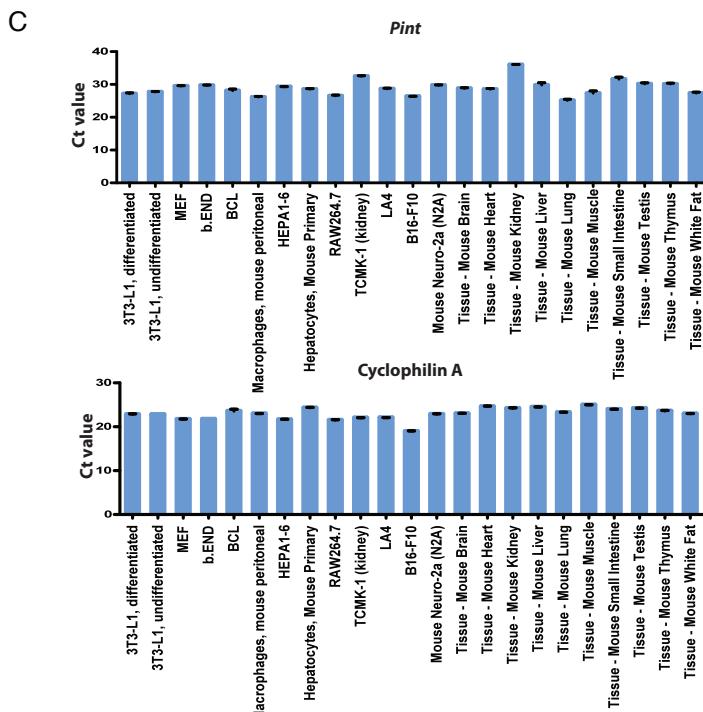
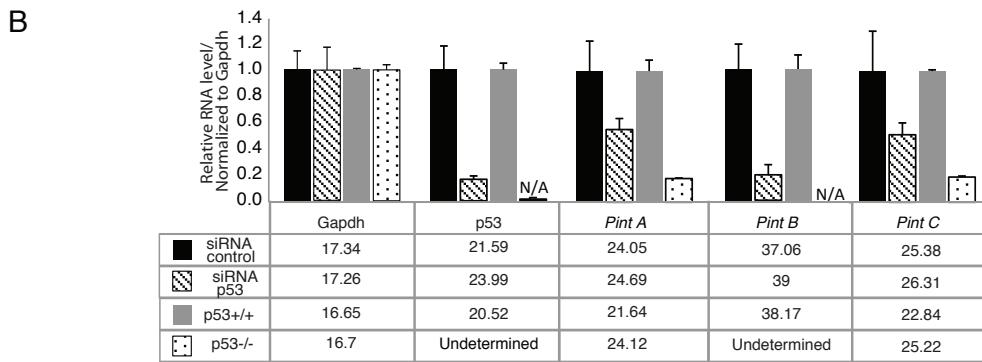
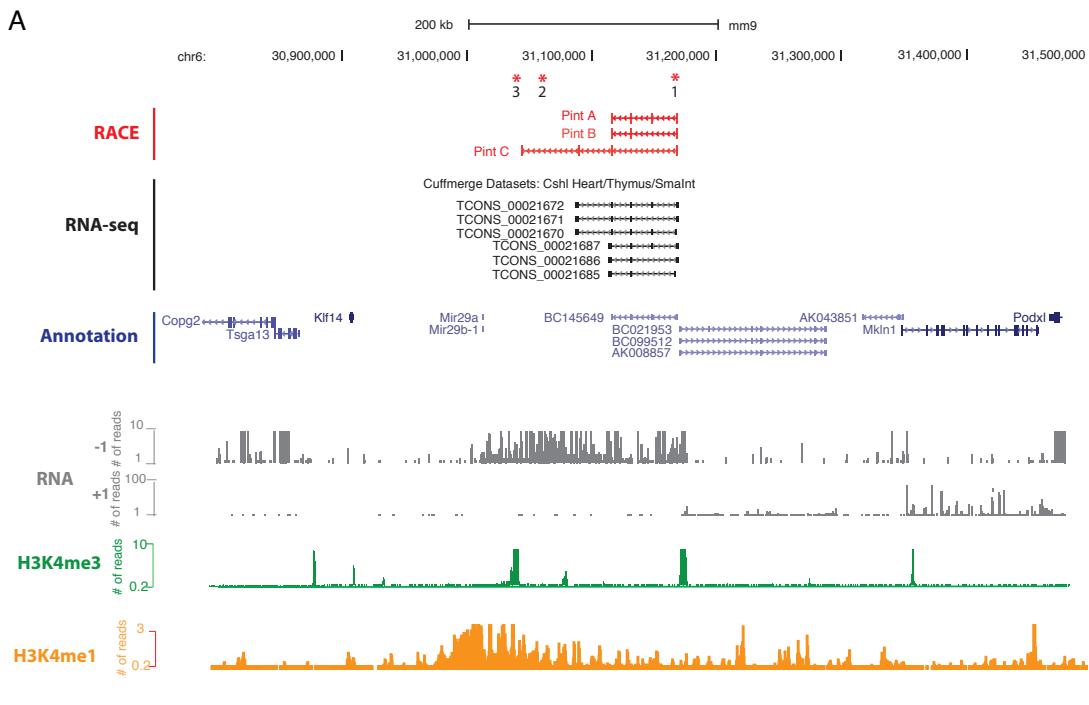
HUMAN qPCR	FORWARD	REVERSE	FIGURE
<i>hGAPDH</i>	GAACCATCGCTCAGACAC	GCCCAATACGACCAAATCC	6A, 6B, 6E, S6C, S6D
<i>PINT</i>	GAACGAGGCAAGGAGCTAAA	AGCAAGGCAGAGAAACTCCA	6A, 6B, 6E, S6C, S6D

ChIP p53 qPCR human	FORWARD	REVERSE	FIGURE
<i>PINT p53RE#1</i>	TTAGCTCCTGCCTCGTTC	TCTACGTGCGCATCTTTC	6C
<i>PINT p53RE#2</i>	TGGGTCACTGACTAGGGAGAA	GGGTCTAGGGTGGAGGAAG	6C
<i>PINT p53RE#3</i>	CCTCGAGATGACACGAGT	GAGGGTGCATGGATCATAGG	6C
<i>PERP p53RE</i>	GCATGTTCACTCATACTAGTTTGCA	GAAAATCCTCTGATGTATTCT	6C
<i>NC6 (control-)</i>	TTCTTA	CAGAGTGTGAAAGGGTGGAA	6C
	GCTCCCTCAGCTAACATC	6	



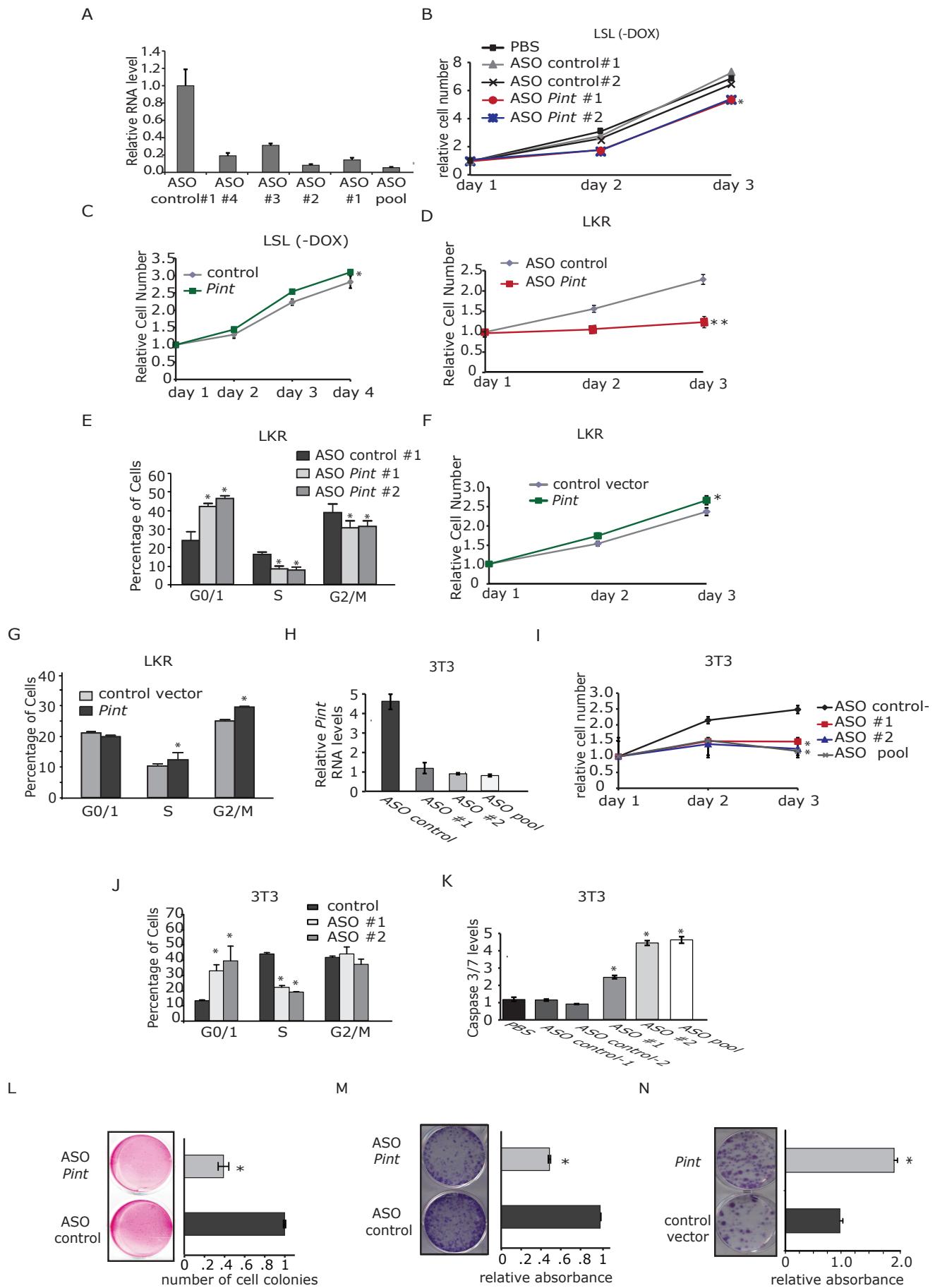
**Figure 1. p53 ChIP-seq data on *PINT* region of mESCs.**

Total p53 and phosphorylated p53 (p53 S18P) ChIP-seq signal from mESCs treated with doxorubicin (red tracks) or untreated (green tracks) in the regions corresponding to *PINT p53RE#1* (A), *p53RE#2* (B) and *p53RE#3* (C). Data were downloaded from [7].



**Figure S2. *Pint* is a ubiquitously expressed lincRNA.**

- (A) Top: Representation of *Pint* isoforms cloned by RACE (red), isoforms determined by Cufflinks analysis of RNA-seq data from heart, thymus and small intestine (black) and annotated transcripts (blue). Bottom: RNA-seq reads form ovary and H3K4me3 and H3K4me1 ChIP-seq (MEFs) data of *Pint* genomic region. Red asterisks indicate the positions of *Pint* p53REs. Data are downloaded from UCSC genome browser [6].
- (B) Relative RNA levels of Gapdh, p53 and *Pint* isoforms in MEFs transfected with siRNA control, p53 siRNA and in p53<sup>+/+</sup> MEFs or p53<sup>-/-</sup>MEFs. The graph represents the RNA levels relative to gapdh and the table shows the qRT-PCR Ct values.
- (C) *Pint A* (top) and housekeeping gene *cyclophilin A* (bottom) expression levels determined by qRT-PCR of 5ng of total RNA from different mouse cell lines and tissues. -RT controls were performed and no meaningful signal was detected.
- (D) *Pint* levels at different times after p53 restoration in lung tumor (top) and sarcoma cell lines (bottom).

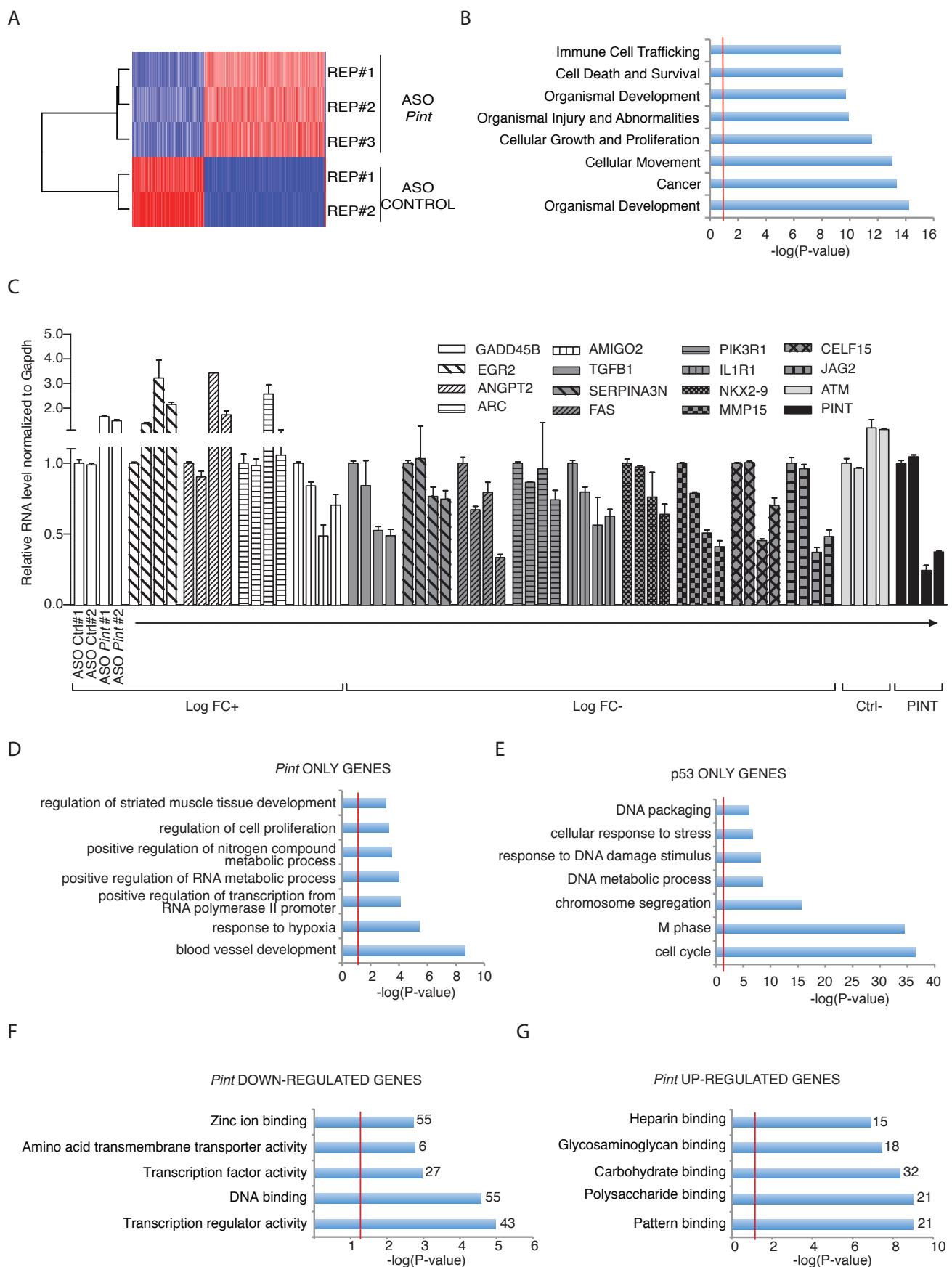


**Figure S3. *Pint* modulates cell proliferation and apoptosis.**

- (A) Relative *Pint* RNA level of p53-restored p53<sup>LSL/LSL</sup> MEFs transfected with the indicated ASOs. *Pint* RNA is normalized to Gapdh and represented relative to the condition ASO control#1.
- (B) Relative number of p53-restored p53<sup>LSL/LSL</sup> MEFs transfected with ASOs for *Pint* inhibition or control ASO.
- (C) Relative number of p53-restored p53<sup>LSL/LSL</sup> MEFs cells stably transduced with a retroviral vector expressing *Pint* or empty vector as control.
- (D) Relative number of LKR cells transfected with a pool of *Pint* targeting ASOs or control ASO. Cells are treated with 150nM Dox from 24h post transfection.
- (E) Percentage of LKR cells in each phase of cell cycle after transfection of two independent *Pint*-targeting ASOs or a control ASO. Cells are treated with 150nM DOX from 24h post transfection for 12h.
- (F) Relative number of LKR cells transfected with a plasmid expressing *Pint* or an empty plamid. Cells are treated with 150nM Dox from 24h post transfection.
- (G) Percentage of LKR cells in each phase of cell cycle after transfection of a plasmid expressing *Pint* or an empty plasmid. Cells are treated with 150nM Dox from 24h post transfection for 12h.
- (H) *Pint* relative levels after transfection of the indicated ASOs in 3T3 MEF cells.
- (I) Relative number of 3T3 MEFs transfected with ASOs for *Pint* inhibition or control ASO and treated with 150nM DOX.
- (J) Percentage of 3T3 MEFs in each phase of the cell cycle after transfection with the indicated ASOs followed with treatment with DOX for 12h.
- (K) Apoptosis levels determined by caspase-3 levels in 3T3 MEFs treated as in (J)
- (L) Growth independent of attachment assay of 3T3 MEFs treated with a pool of *Pint*-targeting ASOs or a control ASO.
- (M) Growth independent of contact assay of cells treated like in (L).

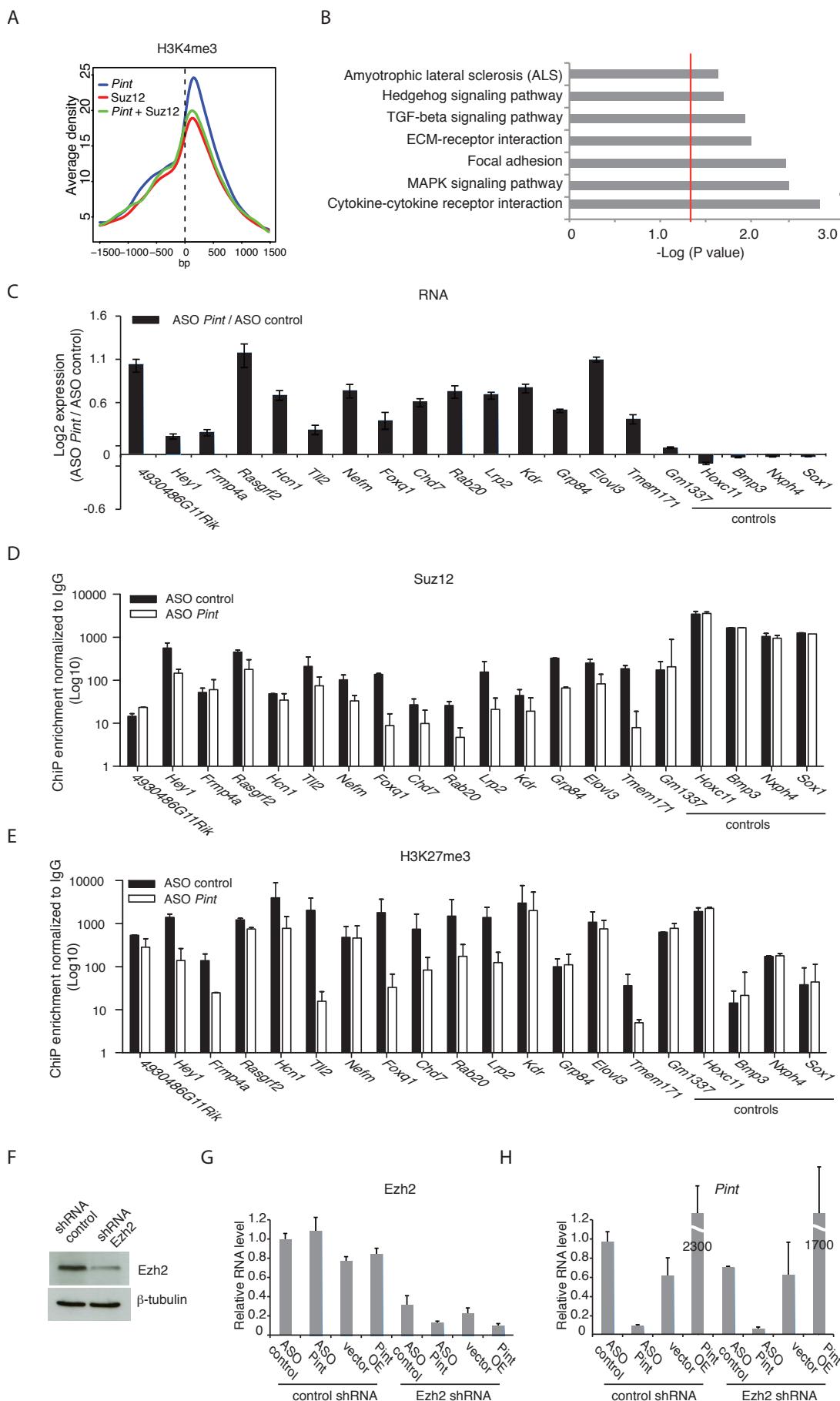
(N) Growth independent of contact assay of 3T3 MEFs transfected with a plasmid expressing *Pint* or an empty plasmid.

Values are average of three biological replicates +/-STD. Asterisks represent statistical significance (\*P<.05, \*\*P<.01, \*\*\*P<.0001).



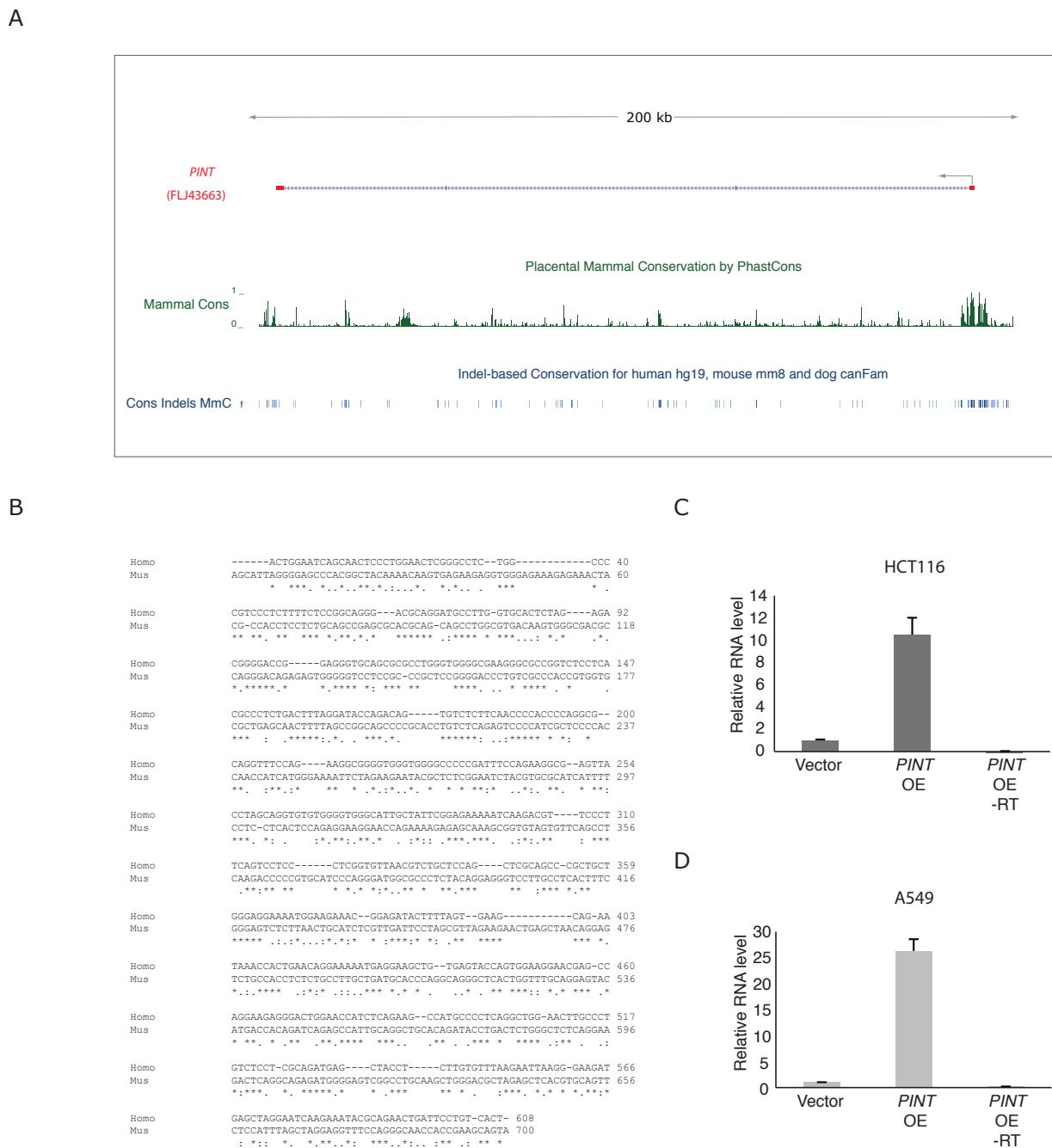
**Figure S4. *Pint* regulates the expression of genes involved in proliferation and survival.**

- (A) Genes affected by *Pint* inhibition in p53-restored DOX-treated p53<sup>LSL/LSL</sup> MEFs (B>3). Colors represent transcripts above (blue) or below (red) the global median scaled to 2-fold activation or repression, respectively.
- (B) Significant biofunctions of genes affected by *Pint* inhibition (B>3). The red line indicates P=0.05.
- (C) Validation by qRT-PCR of expression of genes upon depletion of *Pint* with two independent ASOs (ASO *Pint*#1 and ASO *Pint*#2) compared to two independent control ASOs (ASO Ctrl#1 and ASO Ctrl#2). For each mRNA, values are normalized by Gapdh and represented relatively to the condition ASO ctrl#1. Values are the average of 4 replicates +/-STD.
- (D) Biofunctions of genes regulated by *Pint* but not p53.
- (E) Biofunctions of genes regulated by p53 but not *Pint*.
- (F) Biofunctions of genes downregulated by *Pint*.
- (G) Biofunctions of genes upregulated by *Pint*.



**Figure S5. PRC2 is required for *Pint* function.**

- (A) Average H3K4me3 ChIP-seq signal around the TSS of genes regulated by *Pint* but not bound by Suz12 (blue), genes bound by Suz12 but not regulated by *Pint* (red) and genes regulated by *Pint* and bound by Suz12 (green) in mESCs [9].
- (B) Top significant KEGG pathways of genes regulated by *Pint* and bound by Suz12.
- (C) Relative mRNA level of H3K27me3-regulated genes in DOX-treated p53-reconstituted p53<sup>LSL/LSL</sup> MEFs transfected with *Pint*-ASOs. Values are average of three replicates +/-STD.
- (D) and (E) Relative Suz12 (D) or H3K27me3 (E) enrichment in promoter regions of H3K27me3-regulated genes [32] in DOX-treated p53-reconstituted p53<sup>LSL/LSL</sup> MEFs treated with *Pint*-ASOs or control ASOs determined by ChIP-qPCR. Enrichment values are relative to IgG, and are the average of three biological replicates +/-STD.
- (F) Ezh2 protein levels in Ezh2 shRNA and shRNA control stable cell lines. Beta-tubulin levels are shown as loading control.
- (G) and (H). Relative Ezh2 (G) and *Pint* (H) RNA levels in the shRNA control stable cell line (left) and Ezh2 shRNA cell line (right) treated as indicated. Values are the average of four replicates +/- STD.



### **Figure S6. *Pint* human ortholog.**

(A) Conservation across placental mammalian species determined by PhasCons (green) and indel-based conservation for human, mouse and dog determined by canFam (blue) in *PINT* genomic locus. Data were obtained from UCSC genome browser [6].

(B) Alignment of mouse (*Pint A*) and human *PINT* (FLJ43663) 5' sequences.

(C) and (D) Relative *PINT* levels in HCT116 (C) or A549 (D) cell stable cells lines. Values are normalized by *GAPDH*.

**SUPPLEMENTAL TABLE LEGENDS:**

**Additional file 2, Table S1.** Genomic coordinates and sequences of p53REs found in mouse and human *PINT* genomic loci.

**Additional file 3, Table S2.** Genes affected by *PINT* inhibition by ASO transfection of p53-reconstituted p53<sup>LSL/LSL</sup> MEFs treated with DOX (B>3).

**Additional file 4, Table S3.** Predicted upstream regulators of genes affected by *Pint* knockdown.

**Additional file 5, Table S4.** Genes affected by p53 inhibition by siRNA transfection of p53-reconstituted p53<sup>LSL/LSL</sup> MEFs treated with DOX (B>3).

**Additional file 6, Table S5.** Genes commonly affected by *Pint* and p53 inhibitions.

**Additional file 7, Table S6.** Genes regulated by *Pint* (B>3) found to be bound by Suz12 in mESC [8].

**Additional file 8, Table S7.** Human samples included in this study

***Pint* SEQUENCES:**

> **mus musculus Pint A**

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CCCACGGCTACAAACCAAGTGAGAAGAGGTGGGAGAAAGAGAAACTAGCCACCTCCTCTGCA
GCCGAGCGCACGCAGCAGCAGCCTGGCGTGACAAGTGGGCGACGCCAGGGACAGAGAGTGGGGGT
CCTCCGCCCCGCTCCGGGGACCCTGTCGCCACCGTGGTGCCTGAGCAACTTTAGCCGGCA
GCCCGCACCTGTCTCAGAGTCCCCATCGCTCCCCACCAACCATCATGGGAAAATTCTAGAA
GAATACGCTCTCGGAATCTACGTGCGCATCTTCCCTCACTCCAGAGGAAGGAACCAG
AAAAGAGAGCAAAGCGGTAGTGGTCAGCCTCAAGAACCCCCGTGCATCCAGGGATGGCG
CCCTCTACAGGAGGGTCTTCGCTCAGTTGGAGTCTTAACTGCATCTCGTTGATTCC
TAGCAGTTAGAAGAACTGAGCTAACAGGAGTCTGCCACCTCTGCCTGCTGATGCACCCAG
GCAGGGCTCACTGGTTGCAGGAGTACATGACCACAGATCAGAGCCATTGGCTGCACAGATA
CCTGACTCTGGCTCTCAGGAAGACTCAGGCAGAGATGGGAGTCGGCCTGCAAGCTGGAC
GCTAGAGCTACGTGCAGTTCTCCATTAGCTAGGAGGTTCCAGGGCAACCACCGAAGCAG
TAATTAAAGATGAAGAGCTAAAGTAAGTACTTCCAAACCTGAATCCTGAAGGAGGTGGTC
CGCAGGGCTGGTGCACAGTGTGCACTCTTACTTAACATTAAGTAAATAATTTTAA
TACATTTTGAAAACCTCTGATGAGAGGATACACACTAAATTAGGATGTTCCATGCTCTG
CCTTGATTTGTATCTTTTACCGCGCGACGTATTCTGTATGTACGTACACACCACACA
CACACACACATTATGCTTCCACCAGCAGTCATGGGACCAGGCATTGGGATACCAGGGC
TTAAGGTGTCTTCGGGTTCTGTTGAACGTCTAGCATGCAATGTATATATATACATA
CATACATATATATATACACATTAAAGGCATGCAAACGAGCAACTGCAGAGGCGTCTACAG
TACTTAGCGTGTAGCAGCTCATCCAGGCTCTCCAGGCAGT
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> **mus musculus Pint B**

GCAGCAGCCTGGCGTGACAAGTGGCGACGCCAGGGACAGAGAGTGGGGTCCTCCGCCGC  
 TCCGGGACCTGTCGCCACCCTGGTGCCTGAGCAACTTTAGCCGGAGCCCCCACCT  
 GTCTCAGAGTCCCCATCGCTCCCCACCAACCACATGGGAAAATTCTAGAAGAACGCTCT  
 CGGAATCTACGTGCGCATCTTCTCCTACTCCAGAGGAAGGAACCAGAAAAGAGAGCA  
 AAGCGGTAGTGTTCAGCCTCAAGGCATCTCGTTAGCGTTAGAAGAACGTGAGCT  
 AACAGGAGTCTGCCACCTCTGCCTGCTGATGCACCCAGGCAGGGCTACTGGTTGCAG  
 GAGTACATGACCACAGATCAGAGCATTGCAGGCTGCACAGATACTGACTCTGGCTCTCA  
 GGAAGACTCAGGCAGAGATGGGAGTCGGCTGCAAGCTGGACGCTAGAGCTCACGTGCAG  
 TTCTCCATTAGCTAGGAGG

➤ ***mus musculus Pint C***

AATGATGGACATGATATAATGAAACAACATTGTGGAGAGGAAAGCATTAGGGAGCCCACGG  
 CTACAAAACAAGTGAGAAGAGGTGGGAGAAAGAGAAACTACGCCACCTCTGCAGCCGAG  
 CGCACCGCAGCAGCCTGGCGTGACAAGTGGCGACGCCAGGGACAGAGTGGGGCTCTCCG  
 CCCGCTCCGGGACCTGTCGCCACCCTGGTGCCTGAGCAACTTTAGCCGGCAGCCCCG  
 CACCTGTCTCAGAGTCCCCATCGCTCCCCACCAACCACATGGGAAAATTCTAGAAGAAC  
 GCTCTCGGAATCTACGTGCGCATCTTCTCCTACTCCAGAGGAAGGAACCAGAAAAGA  
 GAGCAAAGCGGTGAGTGTTCAGCCTCAAGGCTGCACAGATACTGACTCTGGCTCTCAGG  
 AAGACTCAGGCAGAGATGGGAGTCGGCTGCAAGCTGGACGCTAGAGCTCACGTGCAGTT  
 CTCCATTAGCTAGGAGGTTCCAGGGCAACCACCGAAGCAGTAATTAAAGATGAAGAGCTA  
 AAAGAGAGAAGAATAGCAGCAACCTGGTCTTTACGGAACACAGTAAGCCACCAAAGAG  
 GTGTGGACAGCCAGCGACCTCCACGGAAATCATAAGGGC

➤ ***Homo sapiens PINT (BC130416)***

➤  
 GCTTGAAAGCCGTGGTATGGTAATTATGTATCAAATGCCCTGGTCTATTCTGTTATTATT  
 GTTTGTCATTCTGTTTCCCAGCGATCTGACTGAACCTCGCAGAGGGACAAATCCAGTTT  
 TCTTTTGACTTTGTCAAACATAACAGGCCTGATAGAAAACCTATTGCTCTCCGGGAAA  
 CAAAGTAGGAGGCCACGAAATGTCAATTAAACAGAGCGTGGGTTGGTGACTIONTAGGAAAGGA  
 TTTGAGGACGCTCCTCTGGCTGGCTCCTATGTCATGAGCACAGGCTCACGCACGCACAG  
 ACACCACGGCTCCGGATGCTGTGGCTCCCCGATCGGGCTCCTGCAGGCCAGAACCCCT  
 CGGGGATGCTCGAGGGCTCCGGTGGGAGGTACGGACGCCGTCGGCCGCCGCC  
 CAGTCCTGCTGTTGTCACATGATGGACATGATATAATGAAACAACATTGTGGAGAGGAAAGCA  
 TTAGGGAGCCCACGGTACAAAAACAAGTGAGTGAGAAGAGGTGGGAGGAAGAGAAACTAC  
 GCCACCTCCCCTGCAGCCGAGTGCACGCAGCAGCCTGGCGTACAAGTGGCGACGCCGGGG  
 GGCAGGGAGCCGGGTCTTGGCCCTGGCCGGGACCCACCGCCACCGCGCGAGGACAA  
 CTTTAGCCGGCAGCCCAGACCAGCGCGCACCTGTCTCCGGAGTCTCCACCGCTCTCCCG  
 ATTCACTCCAGGGAAATTCTCAAGAACGCTCTACAAATCTACGTGCGCATCTTCA  
 TCGCGTCGCGCCGGAGGAAGGAACGAGGCAAGGAGCTAAAGCAGCGTGCCTCAGCCCTG  
 GGGCATTTATTAAATGCTTTACGAGTTAGAAGAGTTGGATAATTGCCATCTGGAGTTTC  
 TCTGCCTGCTGATCTGAGCTCAGACCTGCCAATTACCAAGAGATAATTGATAAACACCCCTCT  
 AACAGCTGAGAGGAAATGGAAGAACGGAGATACTTTAGTGAAGCAGAATAAACCACTGA  
 ACAGGAAAATGAGGAAGCTGTGAGTACCAAGTGGAGGAAGCAGGCCAGGAAGAGGGA

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